FRET-based Quantification of Protein-Protein Interactions using the Opera Phenix High Content Screening System

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1. Abstract
FRET-based imaging assays are widely utilized to study protein-protein interactions or signal transduction processes in living cells. Here, we present a high content imaging assay to study the interaction between the pro-apoptotic protein Bad and the anti-apoptotic protein Bcl-XL in living MCF7 cells. In our assay, Bad was fused to the fluorescent protein Venus serving as the FRET acceptor while Bcl-XL was fused to mCerulean3 acting as the FRET donor.

In high content screening assays, FRET is commonly measured using the sensitized emission method, which requires sequential acquisition of the donor image and the FRET image (donor excitation, acceptor emission). This sequential approach reduces the acquisition speed with conventional high content imaging instrumentation.

In this study presented here, we take advantage of the 4 sCMOS cameras in the Revvity Opera Phenix™ High Content Screening System. With its proprietary Synchrony™ Optics, the system enables simultaneous acquisition of the donor and the FRET image with the option to acquire two additional markers in parallel. Optimal excitation of the Cerulean donor with a 425 nm laser further increased the sensitivity in FRET measurements. Image analysis using the Harmony® High Content Analysis Software allowed an easy-to-use workflow to quantify the FRET efficiency on a pixel-by-pixel basis.

In summary, we have established a fast and robust FRET-based high content imaging assay on the Opera Phenix system that quantifies protein-protein interactions on a pixel-by-pixel basis ($Z' = 0.6$).

2. Assay Principle
MCF-7 breast cancer wild type cells or MCF-7 cells stably expressing the fusion protein mCerulean3-Bcl-XL were grown in Collagen-coated CellCarrier™ Ultra 384-well plates, transferred with three different mVenus reporter constructs (Fig 1) and treated with various concentrations of ABT-737 compound. Following a 15–20 h incubation period in the presence of the compound, a live cell staining was performed using Draq5 and TMRM.

3. Ratiometric Imaging of FRET on the Opera Phenix System
Live cells were imaged on a four camera Opera Phenix system equipped with five lasers (375nm/425nm/488nm/561nm/640nm) in confocal mode using the 40x water immersion objective. Taking advantage of all four cameras, the Draq5, TMRM, Cerulean and FRET (ex Cerulean / em Venus) images were acquired simultaneously, followed by the Venus acceptor image in sequential mode.

4. Image Analysis Strategy using Harmony High Content Analysis Software

5. Comparison of the Three Different FRET Acceptors
Venus-Bad shows the highest NFRET value, as Bad is a specific interaction partner for Bcl-XL. Venus-ActA and Venus alone are not binding specifically to Bcl-XL and serve as negative controls. ActA is localized in the same compartment as Bcl-XL and represents random collisions between the interaction partners. Venus localizes to the cytoplasm and is therefore a localization unmatched control.

6. ABT-737 Disrupts the Bcl-XL-Bad Interaction

7. Summary
Here, we have established a fast and robust high content FRET-based assay to study protein-protein interactions on the Opera Phenix system. The Opera Phenix equipped with five lasers (375nm/425nm/488nm/561nm/640nm) and four cameras is ideally suited for high speed acquisition of CFP/YFP FRET-based assays. The 425nm laser effectively excites the CFP donor, leading to bright FRET signals and maximized signal windows. With its proprietary Synchrony™ Optics, the system enables simultaneous confocal acquisition of the donor and the FRET image with the option to acquire two additional markers in parallel.

The image analysis is based on the easy-to-use building blocks of the Harmony software. Using the Calculate Image feature, a ratiometric image can be calculated using any FRET formula described in the literature. A ratiometric image generated this way represents the FRET efficiency on a per pixel basis, allowing analysis of the exact distribution of the protein complex of interest within the cell.